Claims 39-47 were rejected in the First Office Action under 35 U.S.C. 112, second paragraph as indefinite. Applicant respectfully submits that the claims as amended address these bases of rejection and requests that they be withdrawn.

Claim 48 has been rejected under the judicially created doctrine of obviousness-type double patenting. Applicant attaches a terminal disclaimer to overcome this rejection. Applicant, therefore, requests that this ground of rejection be withdrawn as well. Additionally, while no explanation of the Claim 49 objection (contained in the Office Action Summary) was made in the Office Action, Applicant presumes that the objection is related to Claim 49's dependency on a rejected claim. Applicant, therefore, presumes that the submitted terminal disclaimer will remove any objection to Claim 49 as well.

Claims 29-47 have been rejected under 35 U.S.C. 102(e) as anticipated by the DeLeys reference (U.S. Patent No. 5,891,640). Applicant has amended the claims to eliminate reference to SEQ ID NO. 11. As it appears that the DeLeys reference merely relates to SEQ ID NO. 11, Applicant respectfully submits that this amendment is sufficient to overcome the rejection and respectfully requests that it be withdrawn.

In the event this paper is not timely filed, Applicant hereby petitions for an appropriate extension of time. The fee for this extension may be charged to our Deposit Account No. 01-2300, along with any other fees which may be due with respect to this paper.

Respectfully submitted,

D. Daniel Dzara, II
Registration No. 47,543

ARENT FOX KINTNER PLOTKIN & KAHN, PLLC
1050 Connecticut Avenue, N.W.,
Suite 600
Washington, D.C. 20036-5339
Tel: (202) 857-6000
Fax: (202) 638-4810

Enclosures: Marked Up Copy of Claims
Terminal Disclaimer

MARKED UP COPY OF CLAIMS

--29. (Amended) A peptide suitable for detecting an antibody against hepatitis C virus, consisting of:

(a) an isolated immunologically active amino acid sequence from the hepatitis C virus consisting of 6-22 amino acids from one of SEQ ID NOs: [11-16] 12-16;

(b) optionally, an immunologically inactive spacer region coupled to the immunologically active sequence; and

(c) optionally, a solid phase binding group or a marker group coupled to the spacer region.

32. (Amended) The peptide of claim 29, wherein the immunologically active amino acid sequence consists of 9-20 amino acids from one of SEQ ID NOs: [11-16] 12-16.

39. (Amended) A method of detecting the presence or absence of an antibody against hepatitis C virus in a sample liquid, the method comprising the following steps:

(a) incubating said [a] sample liquid which may contain an antibody against hepatitis C virus with a peptide consisting of: (1) an isolated immunologically active amino acid sequence from the hepatitis C virus consisting of 6-22 amino acids from one of SEQ ID NOs: [11-16] 12-16; (2) optionally, an immunologically inactive spacer region coupled to the immunologically active sequence; and (3) optionally, a solid phase binding group or a marker group coupled to the spacer region; and

(b) detecting any binding between the antibody and the peptide, thereby detecting the presence or absence of the antibody in said sample liquid.

40. The method of claim 39, wherein the peptide consists of [(a), (b) and (c)] (1), (2) and (3).

41. The method of claim 40, wherein [(c)] (3) is a solid phase binding group.

43. (Amended) The method of claim 39, wherein the immunologically active amino acid sequence consists of 9-20 amino acids from one of SEQ ID NOs: [11-16] 12-16.

44. The method of claim 40, wherein [(c)] (3) is a marker group.

45. (Amended) A method of detecting the presence or absence of an antibody against hepatitis C virus in a sample liquid, the method comprising the following steps:

(a) incubating [a] said sample liquid which may contain an antibody against hepatitis C virus with two peptides P1 and P2, wherein [one of] the peptide[s] P1 [and P2] consists of (1) an isolated immunologically active amino acid sequence from the hepatitis C virus consisting of 6-22 amino acids from one of SEQ ID NOs: [11-16] 12-16; (2) an immunologically inactive spacer region coupled to the immunologically active sequence; and (3) a solid phase binding group [or a marker group coupled to the spacer region]; and the peptide P2 consists of (1) an isolated immunologically active amino acid sequence from the hepatitis C virus consisting of 6-22 amino acids from one of SEQ ID NOs: 12-16; (2) optionally, an immunologically inactive spacer region coupled to the immunologically active sequence; and (3) a marker group coupled to the spacer region; and

(b) detecting any binding between the antibody and both of the peptides P1 and P2, thereby detecting the presence or absence of the antibody in said sample liquid.

47. (Amended) The method of claim 45, wherein in each of the peptides P1 and P2 the immunologically active amino acid sequence consists of 9-20 amino acids from one of SEQ ID NOs: [11-16] 12-16.

48. (Amended) A method of detecting the presence or absence of an antibody against hepatitis C virus in a sample, the method comprising the following steps:

(a) incubating a first aliquot of the sample liquid with at least one first immobilized antigen which is specific for a first group of antibodies to be typed, to react the first group antibodies with the at least one first immobilized antigen, wherein the at least one first immobilized antigen consists of: (1) a first isolated immunologically active amino acid sequence from the hepatitis C virus consisting of 6-22 amino acids from one of SEQ ID NOs: 11-16; (2) an immunologically inactive spacer region coupled to the first immunologically active sequence; and (3) a solid phase binding group coupled to the spacer region, and the first group of antibodies is present in an amount which does not exceed the capacity of the at least one first immobilized antigen;

(b) thereafter, separating the first aliquot from step (a) from the at least one first immobilized antigen, and incubating the first aliquot with at least one second immobilized antigen which is specific for a second group of antibodies to be typed, to react the second group of antibodies with the at least one second immobilized antigen, wherein the at least one second immobilized antigen consists of: (1) a second isolated immunologically active amino acid sequence from the hepatitis C virus consisting of 6-22 amino acids from one of SEQ ID NOs: 11-16, wherein the second immunologically active sequence is different than the first immunologically active sequence; (2) an immunologically inactive spacer region coupled to the second immunologically active sequence; and (3) a solid phase binding group coupled to the spacer region;

(c) optionally repeating step (b) with at least one further antigen or antigens, each of which is specific for at least one further group of antibodies to be typed, wherein each of the at least one further antigen or antigens consists of: (1) a further isolated immunologically active amino acid sequence from the hepatitis C virus consisting of 6-

22 amino acids from one of SEQ ID NOs: 11-16, wherein the further immunologically active sequence is different than the first immunologically active sequence and the second immunologically active sequence; (2) an immunologically inactive spacer region coupled to the second immunologically active sequence; and (3) a solid phase binding group coupled to the spacer region, and in each repeated step (b) the at least one further antigen or antigens are incubated separately from the antigen or antigens in a previous step (b);

(d) optionally repeating steps (a) through (c) with a second aliquot of the sample liquid, wherein the sequence of antigens is different than for steps (a) through (c) conducted with the first aliquot;

(e) qualitatively or quantitatively determining the immunological activity of the respective immobilized antigens with the respective groups of antibodies in the sample to be typed; and

(f) typing the antibodies in the sample based on the determining step (e).